MKALRAVLLI LLLSGQPGSS WAQEAGDVDL ELERYSYDDD GDDDDDDDEE

EEEEETNMIP GSRDRAPPLQ CYFCQVLHSG ESCNETQRCS SSKPFCITVI

SHGKTDTGVL TTYSMWCTDT CQPIVKTVDS TQMTQTCCQS TLCNIPPWQS

PQIHNPLGGR ADSPLKGGTR HPQGDRFSHP QVVKVTHPQS DGAHLSKGGK

ANQPQGNGAG FPAGWSKFGN VVLLLTFLTS LWASGA

FIG. 1

```
                                              42
TCTAGCGAACCCCTTCGGTGGACAGAACAGCCTGAGTCAGGATGAAAGCTCTCAGGGCTGTCCTCCTGATCTTGCTACTCAGTGGACAGC
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 90
AGATCGCTTGGGGAAGCCACCTGTCTTGTCGGACTCAGTCCTACTTTCGAGAGTCCCGACAGGAGGACTAGAACGATGAGTCACCTGTCG

  L . R T P S V D R T A . V R (M) K A L R A V L L I L L L S G Q
CAGGGAGCAGCTGGGCACAAGAAGCTGGCGATGTGGACCTGGAGCTAGAGCGCTACAGCTACGATGATGACGGTGATGACGATGATGACG
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 180
GTCCCTCGTCGACCCGTGTTCTTCGACCGCTACACCTGGACCTCGATCTCGCGATGTCGATGCTACTACTGCCACTACTGCTACTACTGC

  P G S S W A Q E A G D V D L E L E R Y S Y D D D D G D D D D D
ATGATGAAGAAGAGGAAGAGGAGGAGACCAACATGATCCCTGGCAGCAGGGACAGAGCACCGCCTCTACAGTGCTACTTCTGCCAAGTGC
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 270
TACTACTTCTTCTCCTTCTCCTCCTCTGGTTGTACTAGGGACCGTCGTCCCTGTCTCGTGGCGGAGATGTCACGATGAAGACGGTTCACG

  D D E E E E E E E T N M I P G S R D R A P P L Q C Y F C Q V
TTCACAGCGGGGAGAGCTGCAACGAGACACAGAGATGCTCCAGCAGCAAGCCCTTCTGTATCACAGTCATCTCCCATGGCAAAACTGACA
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 360
AAGTGTCGCCCCTCTCGACGTTGCTCTGTGTCTCTACGAGGTCGTCGTTCGGGAAGACATAGTGTCAGTAGAGGGTACCGTTTTGACTGT

  L H S G E S C N E T Q R C S S S K P F C I T V I S H G K T D
CAGGTGTCCTGACGACCTACTCCATGTGGTGTACTGATACCTGCCAGCCCATCGTGAAGACAGTGGACAGCACCCAAATGACCCAGACCT
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 450
GTCCACAGGACTGCTGGATGAGGTACACCACATGACTATGGACGGTCGGGTAGCACTTCTGTCACCTGTCGTGGGTTTACTGGGTCTGGA

  T G V L T T Y S M W C T D T C Q P I V K T V D S T Q M T Q T
GTTGCCAGTCCACACTCTGCAATATTCCACCCTGGCAGAGCCCCCAAATCCACAACCCTCTGGGTGGCCGGGCAGACAGCCCCTTGAAGG
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 540
CAACGGTCAGGTGTGAGACGTTATAAGGTGGGACCGTCTCGGGGGTTTAGGTGTTGGGAGACCCACCGGCCCGTCTGTCGGGGAACTTCC

  C C Q S T L C N I P P W Q S P Q I H N P L G G R A D S P L K
GTGGGACCAGACATCCTCAAGGTGACAGGTTTAGCCACCCCCAGGTTGTCAAGGTTACTCATCCTCAGAGTGATGGGGCTCACTTGTCTA
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 630
CACCCTGGTCTGTAGGAGTTCCACTGTCCAAATCGGTGGGGGTCCAACAGTTCCAATGAGTAGGAGTCTCACTACCCCGAGTGAACAGAT

  G G T R H P Q G D R F S H P Q V V K V T H P Q S D Q A H L S
AGGGTGGCAAGGCTAACCAGCCCCAGGGAAATGGGGCCGGATTCCCTGCAGGCTGGAGCAAATTTGGTAACGTAGTTCTCCTGCTCACCT
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 720
TCCCACCGTTCCGATTGGTCGGGGTCCCTTTACCCCGGCCTAAGGGACGTCCGACCTCGTTTAAACCATTGCATCAAGAGGACGAGTGGA

                           749
  K G G K A N Q P Q G N G A G F P A G W S K F G N V V L L L T
TCCTCACCAGTCTGTGGGCATCAGGGGCCTAAAGACTCGTCCTCCCCCAACCAGGACCCTTCAGCCTTTCCTCCCTGACAACCAGCTTCA
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 810
AGGAGTGGTCAGACACCCGTAGTCCCCGGATTTCTGAGCAGGAGGGGGTTGGTCCTGGGAAGTCGGAAAGGAGGGACTGTTGGTCGAAGT

  F L T S L W A S G A . R L V L P Q P G P F S L S S L T T S F
GAGAATAAACTTGAATGTCTTTTGCCATCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGGCCGCC
+---+---+---+---+---+---+---+---+---+---+---> 874
CTCTTATTTGAACTTACAGAAAACGGTAGATTTTTTTTTTTTTTTTTTTTTTTTTTTTCGCCGGCGG

  R E . T . M S F A I . K K K K K K K K K R P P
```

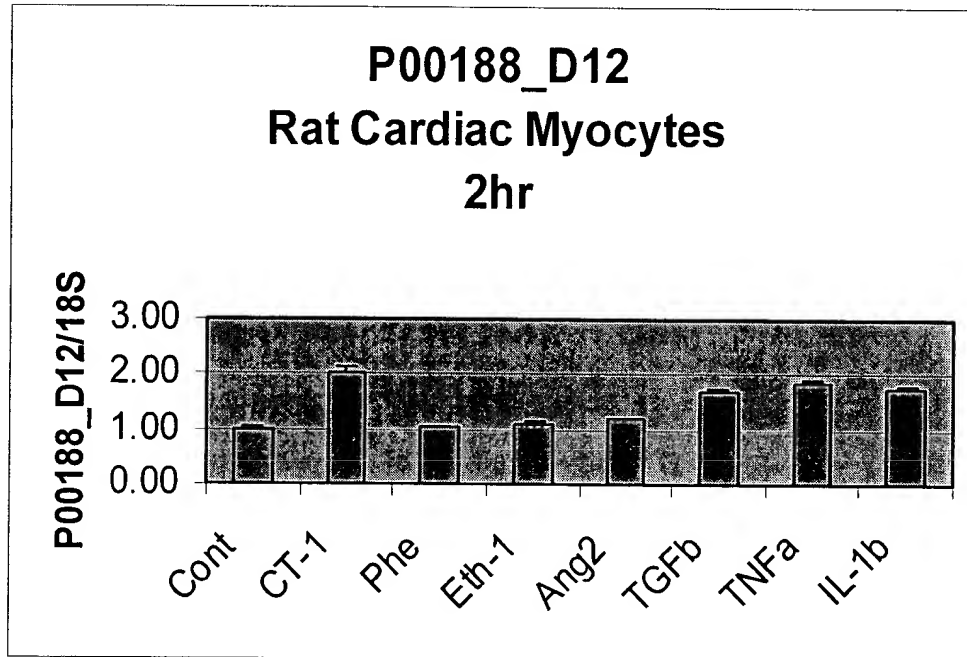**Fig. 2**

Rat Multiple Tissue Northern Blot
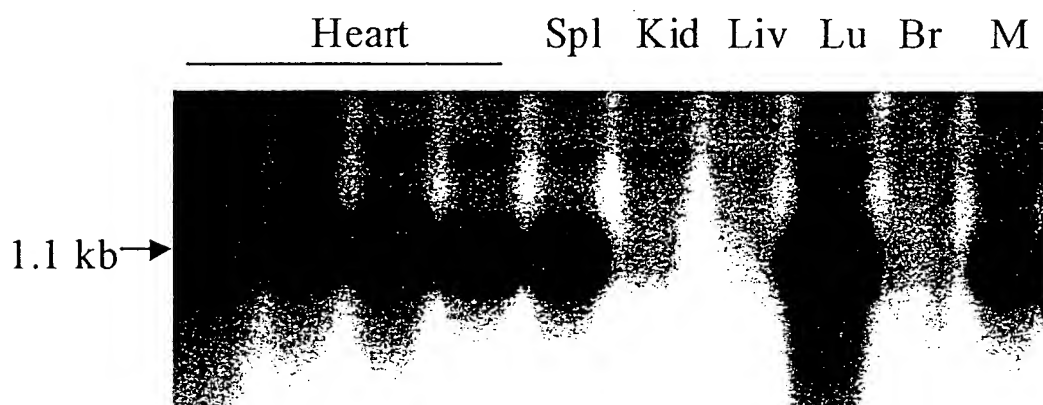
Probe: P00188_D12 rat cDNA

Fig. 3

Fig 4

Expression of P00188_D12 in treated rat cardiac myocytes

A

P00188_D12
Rat Cardiac Myocytes
2hr

P00188_D12/18S

3.00
2.00
1.00
0.00

Cont CT-1 Phe Eth-1 Ang2 TGFb TNFa IL-1b

B

P00188_D12
Rat Cardiac Myocytes
24 hr

P00188_D12/18S

2.00
1.50
1.00
0.50
0.00

Cont CT-1 Phe Eth-1 Ang2 TGFb TNFa IL-1b